

SEQUENCE LISTING

<110> Barber, Elizabeth K

<120> Gene Expression Control Element DNA

<130> 896034605001

<150> US 60/237,079

<151> 2000-09-30

<160> 33

<170> PatentIn version 3.1

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<212> DNA

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<220>

<221> exon

<222> (3)..(137)

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<221> polyA\_site

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Tyr Lys Gly Lys Arg Lys Arg Asn Gly Gln Val Val Lys Leu  
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tga act cag gtg tgc aca att atc agg aac acc cca aaa cca aag tga 95  
Thr Gln Val Cys Thr Ile Ile Arg Asn Thr Pro Lys Pro Lys  
15 20 25

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<211> 996

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<220>

<221> exon

<222> (1)..(996)

<223>

<220>

<221> misc\_feature

<222> (710)..(996)

<223> Nucleotides 710-996 are homologous to a portion of human dystrophin DNA in the region of exon 79 except that nucleotides 860-996 are inverted in comparison to the orientation of the same sequence in the dystrophin DNA

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Val Val Leu Ile Val Lys Lys Met Phe Val Asn Thr Ser Arg Glu  
1 5 10 15

taa gta atc aat caa tca ctc ata gcc aag gtg gaa aag atg tat ccc 96  
Val Ile Asn Gln Ser Leu Ile Ala Lys Val Glu Lys Met Tyr Pro

20

25

30

atc atg gaa tat tcc tgt tct gat aga aat ctt gtg ctt atc tat gga	144																																																																																																										
Ile Met Glu Tyr Ser Cys Ser Asp Arg Asn Leu Val Leu Ile Tyr Gly																																																																																																											
35	40		45	att ctt ttg ata tat att tac att ggg aac ctg aat gta gct tga cat	192	Ile Leu Leu Ile Tyr Ile Tyr Gly Asn Leu Asn Val Ala His		50	55		60	ttt tcc atg taa aca cca gta gcc tga tcc aac att aag ctg ata cta	240	Phe Ser Met Thr Pro Val Ala Ser Asn Ile Lys Leu Ile Leu		65	70		75	aca aac aac gtg taa tgg ctt cat taa taa ggc ttt gct tct tcc tgg	288	Thr Asn Asn Val Trp Leu His Gly Phe Ala Ser Ser Trp		80	85	aaa ctg gtg aaa aat caa acc ttg ttg tgt aca ccc tcg atg cag ctt	336	Lys Leu Val Lys Asn Gln Thr Leu Leu Cys Thr Pro Ser Met Gln Leu		90	95		100	ctg tgt tgt ctt cac cca gaa atg ggg aat gat ttc cca aat ggc aaa	384	Leu Cys Cys Leu His Pro Glu Met Gly Asn Asp Phe Pro Asn Gly Lys		105	110		115		120	gaa aca gag tga tgc tat cta tct gca cct ttt gta aag tct gtc ttt	432	Glu Thr Glu Cys Tyr Leu Ser Ala Pro Phe Val Lys Ser Val Phe		125	130		135	ctt tct ctt tgt ttt cca gga cac aat gta gga agt ctt ttc cac atg	480	Leu Ser Leu Cys Phe Pro Gly His Asn Val Gly Ser Leu Phe His Met		140	145		150	gca gat gat ttg ggc aga gcg atg gag tcc tta gta tca gtc atg aca	528	Ala Asp Asp Leu Gly Arg Ala Met Glu Ser Leu Val Ser Val Met Thr		155	160		165	gat gaa gaa gga gca gaa taa atg ttt tac aac tcc tga ttc ccg cat	576	Asp Glu Glu Gly Ala Glu Met Phe Tyr Asn Ser Phe Pro His		170	175		180	ggt ttt tat aat att cat aca aca aag agg att aga cag taa gag ttt	624	Gly Phe Tyr Asn Ile His Thr Thr Lys Arg Ile Arg Gln Glu Phe		185	190		195	aca aga aat aaa tct ata ttt ttg tga agg gta gtg gta tta tac tgt	672	Thr Arg Asn Lys Ser Ile Phe Leu Arg Val Val Val Leu Tyr Cys		200	205		210	aga ttt cag tag ttt cta agt ctg tta ttg ttt tgt taa caa tgg cag	720	Arg Phe Gln Phe Leu Ser Leu Leu Phe Cys Gln Trp Gln		215	220		225	gtt tta cac gtc tat gca att gta caa aaa agt tat aag aaa act aca	768	Val Leu His Val Tyr Ala Ile Val Gln Lys Ser Tyr Lys Lys Thr Thr		230	235		240
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att ctt ttg ata tat att tac att ggg aac ctg aat gta gct tga cat	192																																																																																																										
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50	55		60	ttt tcc atg taa aca cca gta gcc tga tcc aac att aag ctg ata cta	240	Phe Ser Met Thr Pro Val Ala Ser Asn Ile Lys Leu Ile Leu		65	70		75	aca aac aac gtg taa tgg ctt cat taa taa ggc ttt gct tct tcc tgg	288	Thr Asn Asn Val Trp Leu His Gly Phe Ala Ser Ser Trp		80	85	aaa ctg gtg aaa aat caa acc ttg ttg tgt aca ccc tcg atg cag ctt	336	Lys Leu Val Lys Asn Gln Thr Leu Leu Cys Thr Pro Ser Met Gln Leu		90	95		100	ctg tgt tgt ctt cac cca gaa atg ggg aat gat ttc cca aat ggc aaa	384	Leu Cys Cys Leu His Pro Glu Met Gly Asn Asp Phe Pro Asn Gly Lys		105	110		115		120	gaa aca gag tga tgc tat cta tct gca cct ttt gta aag tct gtc ttt	432	Glu Thr Glu Cys Tyr Leu Ser Ala Pro Phe Val Lys Ser Val Phe		125	130		135	ctt tct ctt tgt ttt cca gga cac aat gta gga agt ctt ttc cac atg	480	Leu Ser Leu Cys Phe Pro Gly His Asn Val Gly Ser Leu Phe His Met		140	145		150	gca gat gat ttg ggc aga gcg atg gag tcc tta gta tca gtc atg aca	528	Ala Asp Asp Leu Gly Arg Ala Met Glu Ser Leu Val Ser Val Met Thr		155	160		165	gat gaa gaa gga gca gaa taa atg ttt tac aac tcc tga ttc ccg cat	576	Asp Glu Glu Gly Ala Glu Met Phe Tyr Asn Ser Phe Pro His		170	175		180	ggt ttt tat aat att cat aca aca aag agg att aga cag taa gag ttt	624	Gly Phe Tyr Asn Ile His Thr Thr Lys Arg Ile Arg Gln Glu Phe		185	190		195	aca aga aat aaa tct ata ttt ttg tga agg gta gtg gta tta tac tgt	672	Thr Arg Asn Lys Ser Ile Phe Leu Arg Val Val Val Leu Tyr Cys		200	205		210	aga ttt cag tag ttt cta agt ctg tta ttg ttt tgt taa caa tgg cag	720	Arg Phe Gln Phe Leu Ser Leu Leu Phe Cys Gln Trp Gln		215	220		225	gtt tta cac gtc tat gca att gta caa aaa agt tat aag aaa act aca	768	Val Leu His Val Tyr Ala Ile Val Gln Lys Ser Tyr Lys Lys Thr Thr		230	235		240								
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aga ttt cag tag ttt cta agt ctg tta ttg ttt tgt taa caa tgg cag	720																																																																																																										
Arg Phe Gln Phe Leu Ser Leu Leu Phe Cys Gln Trp Gln																																																																																																											
215	220		225	gtt tta cac gtc tat gca att gta caa aaa agt tat aag aaa act aca	768	Val Leu His Val Tyr Ala Ile Val Gln Lys Ser Tyr Lys Lys Thr Thr		230	235		240																																																																																																
	225																																																																																																										
gtt tta cac gtc tat gca att gta caa aaa agt tat aag aaa act aca	768																																																																																																										
Val Leu His Val Tyr Ala Ile Val Gln Lys Ser Tyr Lys Lys Thr Thr																																																																																																											
230	235		240																																																																																																								
	240																																																																																																										

tgt aaa atc ttg ata gct aaa taa ctt gcc att tct tta tat gga acg 816  
Cys Lys Ile Leu Ile Ala Lys Leu Ala Ile Ser Leu Tyr Gly Thr  
245 250 255

cat ttt ggg ttg ttt aaa aat tta taa cag tta taa aga aag aat tat 864  
His Phe Gly Leu Phe Lys Asn Leu Gln Leu Arg Lys Asn Tyr  
260 265 270

aaa gga aaa aga aaa taa cgc aat gga caa gtg gtg aag ctg tga act 912  
Lys Gly Lys Arg Lys Arg Asn Gly Gln Val Val Lys Leu Thr  
275 280

cag gtg tgc aca att atc agg aac acc cca aaa cca aag tga ggt aga 960  
Gln Val Cys Thr Ile Ile Arg Asn Thr Pro Lys Pro Lys Gly Arg  
285 290 295

aat agc atg aga agc cgt gtt tga tgt taa tta att 996  
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22

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Ile Tyr Ile Tyr Ile Gly Asn Leu Asn Met Lys Lys Glu Gln Asn Lys  
35 40 45

Cys Phe Thr Thr Pro Asp Ser Arg Met Val Phe Ile Ile Phe Ile Gln  
50 55 60

Gln Arg Gly Leu Asp Ser Lys Ser Leu Gln Glu Ile Asn Leu Tyr Phe  
65 70 75 80

Cys Glu Gly Phe Tyr Thr Ser Met Gln Leu Tyr Lys Lys Val Ile Arg  
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Lys Leu His Lys Ile Thr Gln Trp Thr Arg Thr Pro Gln Asn Gln Ser  
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Glu Val Glu Ile Ala  
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35 40 45

Gly Asn Leu Asn Val Ala Arg His Phe Ser Met Lys Thr Pro Val Ala  
50 55 60

Arg Ser Asn Ile Lys Leu Ile Leu Thr Asn Asn Val Lys Trp Leu His  
65 70 75 80

Lys Lys Gly Phe Ala Ser Ser Trp Lys Leu Val Lys Asn Gln Thr Leu  
85 90 95

Leu Cys Thr Pro Ser Met Gln Leu Leu Cys Cys Leu His Pro Glu Met  
100 105 110

Gly Asn Asp Phe Pro Asn Gly Lys Glu Thr Glu Arg Cys Tyr Leu Ser  
115 120 125

Ala Pro Phe Val Lys Ser Val Phe Leu Ser Leu Cys Phe Pro Gly His  
130 135 140

Asn Val Gly Ser Leu Phe His Met Ala Asp Asp Leu Gly Arg Ala Met  
145 150 155 160

Glu Ser Leu Val Ser Val Met Thr Asp Glu Glu Gly Ala Glu Lys Met  
165 170 175

Phe Tyr Asn Ser Arg Phe Pro His Gly Phe Tyr Asn Ile His Thr Thr  
180 185 190

Lys Arg Ile Arg Gln Lys Glu Phe Thr Arg Asn Lys Ser Ile Phe Leu  
195 200 205

Arg Arg Val Val Val Leu Tyr Cys Arg Phe Gln Lys Phe Leu Ser Leu  
210 215 220

Leu Leu Phe Cys Lys Gln Trp Gln Val Leu His Val Tyr Ala Ile Val  
225 230 235 240

Gln Lys Ser Tyr Lys Lys Thr Thr Cys Lys Ile Leu Ile Ala Lys Lys  
245 250 255

Leu Ala Ile Ser Leu Tyr Gly Thr His Phe Gly Leu Phe Lys Asn Leu  
260 265 270

Lys Gln Leu Lys Arg Lys Asn Tyr Lys Gly Lys Arg Lys Lys Arg Asn  
275 280 285

Gly Gln Val Val Lys Leu Arg Thr Gln Val Cys Thr Ile Ile Arg Asn  
290 295 300

Thr Pro Lys Pro Lys Arg Gly Arg Asn Ser Met Arg Ser Arg Val Arg  
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Cys Lys Leu Ile

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att att att ttc aac cca agt aaa agc aga gag aaa ata gcc acc tcc 96  
 Ile Ile Ile Phe Asn Pro Ser Lys Ser Arg Glu Lys Ile Ala Thr Ser  
 20 25 30

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acc ata gcc tca gaa gca agc caa cag cct gaa aca gct ttg aaa tga 144
Thr Ile Ala Ser Glu Ala Ser Gln Gln Pro Glu Thr Ala Leu Lys
35          40          45

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aaa gtt ggt gtg gcg gtg atg gtg gca gtg ata atg gtg acc gat ggt 192
Lys Val Gly Val Ala Val Met Val Ala Val Ile Met Val Thr Asp Gly
      50                  55                  60

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tgg gtg ctg gtg atg gta gtg gta gtt gtg aag gtg gtg atg  
 Trp Val Leu Val Met Val Val Val Val Val Lys Val Val Val Met  
 65 70 75